

SEQUENCE LISTING

<110> TOYO BOSEKI KABUSHIKI KAISHA

<120> MODIFIED THERMOSTABLE DNA POLYMERASE

<130> 000053

<140>

<141>

<150> 2000-138796

<151> 2000-05-11

<160> 28

<170> PatentIn Ver. 2.1

<210> 1

<211> 5342

<212> DNA

<213> Pyrococcus kodakaraensis

<220>

<221> CDS

<222> (156)..(5165)

<223> 1374-2453 intron, 2709-4316 intron

<400> 1

gcttgagggc ctgcggttat gggacgttgc agtttgcgcc tactcaaaga tgccggtttt 60

ataacggaga aaaatgggga gctattacga tctctccttg atgtgggggt tacaataaag 120

cctggattgt tctacaagat tatgggggat gaaag atg atc ctc gac act gac 173

Met Ile Leu Asp Thr Asp

1

5

tac ata acc gag gat gga aag cct gtc ata aga att ttc aag aag gaa 221

Tyr Ile Thr Glu Asp Gly Lys Pro Val Ile Arg Ile Phe Lys Lys Glu

10

15

20

aac ggc gag ttt aag att gag tac gac cgg act ttt gaa ccc tac ttc 269

Asn Gly Glu Phe Lys Ile Glu Tyr Asp Arg Thr Phe Glu Pro Tyr Phe

25

30

35

tac gcc ctc ctg aag gac gat tct gcc att gag gaa gtc aag aag ata 317

Tyr Ala Leu Leu Lys Asp Asp Ser Ala Ile Glu Glu Val Lys Lys Ile

40

45

50

acc gcc gag agg cac ggg acg gtt gta acg gtt aag cgg gtt gaa aag 365

Thr Ala Glu Arg His Gly Thr Val Val Thr Val Lys Arg Val Glu Lys

55

60

65

70

gtt cag aag aag ttc ctc ggg aga cca gtt gag gtc tgg aaa ctc tac 413

Val Gln Lys Lys Phe Leu Gly Arg Pro Val Glu Val Trp Lys Leu Tyr

75

80

85

ttt act cat ccg cag gac gtc cca gcg ata agg gac aag ata cga gag 461

Phe Thr His Pro Gln Asp Val Pro Ala Ile Arg Asp Lys Ile Arg Glu

F00150, 2262860

90	95	100	
cat ggg gca gtt att gac atc tac gag tac gac ata ccc ttc gcc aag			509
His Gly Ala Val Ile Asp Ile Tyr Glu Tyr Asp Ile Pro Phe Ala Lys			
105	110	115	
cgc tac ctc ata gac aag gga tta gtg cca atg gaa ggc gac gag gag			557
Arg Tyr Leu Ile Asp Lys Gly Leu Val Pro Met Glu Gly Asp Glu Glu			
120	125	130	
ctg aaa atg ctc gcc ttc gac att gaa act ctc tac cat gag ggc gag			605
Leu Lys Met Leu Ala Phe Asp Ile Glu Thr Leu Tyr His Glu Gly Glu			
135	140	145	150
gag ttc gcc gag ggg cca atc ctt atg ata agc tac gcc gac gag gaa			653
Glu Phe Ala Glu Gly Pro Ile Leu Met Ile Ser Tyr Ala Asp Glu Glu			
155	160	165	
ggg gcc agg gtg ata act tgg aag aac gtg gat ctc ccc tac gtt gac			701
Gly Ala Arg Val Ile Thr Trp Lys Asn Val Asp Leu Pro Tyr Val Asp			
170	175	180	
gtc gtc tcg acg gag agg gag atg ata aag cgc ttc ctc cgt gtt gtg			749
Val Val Ser Thr Glu Arg Glu Met Ile Lys Arg Phe Leu Arg Val Val			
185	190	195	

095923 051001
T00T50" 2229860

aag gag aaa gac ccg gac gtt ctc ata acc tac aac ggc gac aac ttc 797

Lys Glu Lys Asp Pro Asp Val Leu Ile Thr Tyr Asn Gly Asp Asn Phe

200

205

210

gac ttc gcc tat ctg aaa aag cgc tgt gaa aag ctc gga ata aac ttc 845

Asp Phe Ala Tyr Leu Lys Lys Arg Cys Glu Lys Leu Gly Ile Asn Phe

215

220

225

230

gcc ctc gga agg gat gga agc gag ccg aag att cag agg atg ggc gac 893

Ala Leu Gly Arg Asp Gly Ser Glu Pro Lys Ile Gln Arg Met Gly Asp

235

240

245

agg ttt gcc gtc gaa gtg aag gga cgg ata cac ttc gat ctc tat cct 941

Arg Phe Ala Val Glu Val Lys Gly Arg Ile His Phe Asp Leu Tyr Pro

250

255

260

gtg ata aga cgg acg ata aac ctg ccc aca tac acg ctt gag gcc gtt 989

Val Ile Arg Arg Thr Ile Asn Leu Pro Thr Tyr Thr Leu Glu Ala Val

265

270

275

tat gaa gcc gtc ttc ggt cag ccg aag gag aag gtt tac gct gag gaa 1037

Tyr Glu Ala Val Phe Gly Gln Pro Lys Glu Lys Val Tyr Ala Glu Glu

280

285

290

005592 051001

295 300 305 310

315 320 325

330 335 340

345 350 355

360 365 370

375 380 385 390

gag ccc gag aga ggg ttg tgg gag aac ata gfg tac cta gat ttt aga 1373

Glu Pro Glu Arg Gly Leu Trp Glu Asn Ile Val Tyr Leu Asp Phe Arg

395

400

405

tgc cat cca gcc gat acg aag gtt gtc gtc aag ggg aag ggg att ata 1421

Cys His Pro Ala Asp Thr Lys Val Val Val Lys Gly Lys Gly Ile Ile

410

415

420

aac atc agc gag gtt cag gaa ggt gac tat gtc ctt ggg att gac ggc 1469

Asn Ile Ser Glu Val Gln Glu Gly Asp Tyr Val Leu Gly Ile Asp Gly

425

430

435

tgg cag aga gtt aga aaa gta tgg gaa tac gac tac aaa ggg gag ctt 1517

Trp Gln Arg Val Arg Lys Val Trp Glu Tyr Asp Tyr Lys Gly Glu Leu

440

445

450

gta aac ata aac ggg tta aag tgt acg ccc aat cat aag ctt ccc gtt 1565

Val Asn Ile Asn Gly Leu Lys Cys Thr Pro Asn His Lys Leu Pro Val

455

460

465

470

gtt aca aag aac gaa cga caa acg aga ata aga gac agt ctt gct aag 1613

Val Thr Lys Asn Glu Arg Gln Thr Arg Ile Arg Asp Ser Leu Ala Lys

475

480

485

tct ttc ctt act aaa aaa gtt aag ggc aag ata ata acc act ccc ctt 1661

Ser Phe Leu Thr Lys Lys Val Lys Gly Lys Ile Ile Thr Thr Pro Leu

00552922 051001

490	495	500	
ttc tat gaa ata ggc aga gcg aca agt gag aat att cca gaa gaa gag 1709			
Phe Tyr Glu Ile Gly Arg Ala Thr Ser Glu Asn Ile Pro Glu Glu Glu			
505	510	515	
gtt ctc aag gga gag ctc gct ggc ata cta ttg gct gaa gga acg ctc 1757			
Val Leu Lys Gly Glu Leu Ala Gly Ile Leu Leu Ala Glu Gly Thr Leu			
520	525	530	
ttg agg aaa gac gtt gaa tac ttt gat tca tcc cgc aaa aaa cgg agg 1805			
Leu Arg Lys Asp Val Glu Tyr Phe Asp Ser Ser Arg Lys Lys Arg Arg			
535	540	545	550
att tca cac cag tat cgt gtt gag ata acc att ggg aaa gac gag gag 1853			
Ile Ser His Gln Tyr Arg Val Glu Ile Thr Ile Gly Lys Asp Glu Glu			
555	560	565	
gag ttt agg gat cgt atc aca tac att ttt gag cgt ttg ttt ggg att 1901			
Glu Phe Arg Asp Arg Ile Thr Tyr Ile Phe Glu Arg Leu Phe Gly Ile			
570	575	580	
act cca agc atc tcg gag aag aaa gga act aac gca gta aca ctc aaa 1949			
Thr Pro Ser Ile Ser Glu Lys Lys Gly Thr Asn Ala Val Thr Leu Lys			
585	590	595	

0936292 054001
100750" 22529860

gtt gcg aag aag aat gtt tat ctt aaa gtc aag gaa att atg gac aac 1997

Val Ala Lys Lys Asn Val Tyr Leu Lys Val Lys Glu Ile Met Asp Asn

600

605

610

ata gag tcc cta cat gcc ccc tcg gtt ctc agg gga ttc ttc gaa ggc 2045

Ile Glu Ser Leu His Ala Pro Ser Val Leu Arg Gly Phe Phe Glu Gly

615

620

625

630

gac ggt tca gta aac agg gtt agg agg agt att gtt gca acc cag ggt 2093

Asp Gly Ser Val Asn Arg Val Arg Arg Ser Ile Val Ala Thr Gln Gly

635

640

645

aca aag aac gag tgg aag att aaa ctg gtg tca aaa ctg ctc tcc cag 2141

Thr Lys Asn Glu Trp Lys Ile Lys Leu Val Ser Lys Leu Leu Ser Gln

650

655

660

ctt ggt atc cct cat caa acg tac acg tat cag tat cag gaa aat ggg 2189

Leu Gly Ile Pro His Gln Thr Tyr Thr Tyr Gln Tyr Gln Glu Asn Gly

665

670

675

aaa gat cgg agc agg tat ata ctg gag ata act gga aag gac gga ttg 2237

Lys Asp Arg Ser Arg Tyr Ile Leu Glu Ile Thr Gly Lys Asp Gly Leu

680

685

690

09652933 051001

ata ctg ttc caa aca ctc att gga ttc atc agt gaa aga aag aac gct 2285

Ile Leu Phe Gln Thr Leu Ile Gly Phe Ile Ser Glu Arg Lys Asn Ala

695 700 705 710

ctg ctt aat aag gca ata tct cag agg gaa atg aac aac ttg gaa aac 2333

Leu Leu Asn Lys Ala Ile Ser Gln Arg Glu Met Asn Asn Leu Glu Asn

715 720 725

aat gga ttt tac agg ctc agt gaa ttc aat gtc agc acg gaa tac tat 2381

Asn Gly Phe Tyr Arg Leu Ser Glu Phe Asn Val Ser Thr Glu Tyr Tyr

730 735 740

gag ggc aag gtc tat gac tta act ctt gaa gga act ccc tac tac ttt 2429

Glu Gly Lys Val Tyr Asp Leu Thr Leu Glu Gly Thr Pro Tyr Tyr Phe

745 750 755

gcc aat ggc ata ttg acc cat aac tcc ctg tac ccc tca atc atc atc 2477

Ala Asn Gly Ile Leu Thr His Asn Ser Leu Tyr Pro Ser Ile Ile Ile

760 765 770

acc cac aac gtc tcg ccg gat acg ctc aac aga gaa gga tgc aag gaa 2525

Thr His Asn Val Ser Pro Asp Thr Leu Asn Arg Glu Gly Cys Lys Glu

775 780 785 790

tat gac gtt gcc cca cag gtc ggc cac cgc ttc tgc aag gac ttc cca 2573

09852922 "051001"

Tyr Asp Val Ala Pro Gln Val Gly His Arg Phe Cys Lys Asp Phe Pro

795

800

805

gga ttt atc ccg agc ctg ctt gga gac ctc cta gag gag agg cag aag 2621

Gly Phe Ile Pro Ser Leu Leu Gly Asp Leu Leu Glu Glu Arg Gln Lys

810

815

820

ata aag aag aag atg aag gcc acg att gac ccg atc gag agg aag ctc 2669

Ile Lys Lys Lys Met Lys Ala Thr Ile Asp Pro Ile Glu Arg Lys Leu

825

830

835

ctc gat tac agg cag agg gcc atc aag atc ctg gca aac agc atc cta 2717

Leu Asp Tyr Arg Gln Arg Ala Ile Lys Ile Leu Ala Asn Ser Ile Leu

840

845

850

ccc gag gaa tgg ctt cca gtc ctc gag gaa ggg gag gtt cac ttc gtc 2765

Pro Glu Glu Trp Leu Pro Val Leu Glu Glu Gly Glu Val His Phe Val

855

860

865

870

agg att gga gag ctc ata gac cgg atg atg gag gaa aat gct ggg aaa 2813

Arg Ile Gly Glu Leu Ile Asp Arg Met Met Glu Glu Asn Ala Gly Lys

875

880

885

gta aag aga gag ggc gag acg gaa gtg ctt gag gtc agt ggg ctt gaa 2861

Val Lys Arg Glu Gly Glu Thr Glu Val Leu Glu Val Ser Gly Leu Glu

890	895	900	
gtc ccg tcc ttt aac agg aga act aac aag gcc gag ctc aag aga gta			2909
Val Pro Ser Phe Asn Arg Arg Thr Asn Lys Ala Glu Leu Lys Arg Val			
905	910	915	
aag gcc ctg att agg cac gat tat tct ggc aag gtc tac acc atc aga			2957
Lys Ala Leu Ile Arg His Asp Tyr Ser Gly Lys Val Tyr Thr Ile Arg			
920	925	930	
ctg aag tcg ggg agg aga ata aag ata acc tct ggc cac agc ctc ttc			3005
Leu Lys Ser Gly Arg Arg Ile Lys Ile Thr Ser Gly His Ser Leu Phe			
935	940	945	950
tct gtg aga aac ggg gag ctc gtt gaa gtt acg ggc gat gaa cta aag			3053
Ser Val Arg Asn Gly Glu Leu Val Glu Val Thr Gly Asp Glu Leu Lys			
955	960	965	
cca ggt gac ctc gtt gca gtc ccg cgg aga ttg gag ctt cct gag aga			3101
Pro Gly Asp Leu Val Ala Val Pro Arg Arg Leu Glu Leu Pro Glu Arg			
970	975	980	
aac cac gtg ctg aac ctc gtt gaa ctg ctc ctt gga acg cca gaa gaa			3149
Asn His Val Leu Asn Leu Val Glu Leu Leu Leu Gly Thr Pro Glu Glu			
985	990	995	

gaa act ttg gac atc gtc atg acg atc cca gtc aag ggt aag aag aac 3197

Glu Thr Leu Asp Ile Val Met Thr Ile Pro Val Lys Gly Lys Lys Asn

1000

1005

1010

ttc ttt aaa ggg atg ctc agg act ttg cgc tgg att ttc gga gag gaa 3245

Phe Phe Lys Gly Met Leu Arg Thr Leu Arg Trp Ile Phe Gly Glu Glu

1015

1020

1025

1030

aag agg ccc aga acc gcg aga cgc tat ctc agg cac ctt gag gat ctg 3293

Lys Arg Pro Arg Thr Ala Arg Arg Tyr Leu Arg His Leu Glu Asp Leu

1035

1040

1045

ggc tat gtc cgg ctt aag aag atc ggc tac gaa gtc ctc gac tgg gac 3341

Gly Tyr Val Arg Leu Lys Lys Ile Gly Tyr Glu Val Leu Asp Trp Asp

1050

1055

1060

tca ctt aag aac tac aga agg ctc tac gag gcg ctt gtc gag aac gtc 3389

Ser Leu Lys Asn Tyr Arg Arg Leu Tyr Glu Ala Leu Val Glu Asn Val

1065

1070

1075

aga tac aac ggc aac aag agg gag tac ctc gtt gaa ttc aat tcc atc 3437

Arg Tyr Asn Gly Asn Lys Arg Glu Tyr Leu Val Glu Phe Asn Ser Ile

1080

1085

1090

100150"2252950

1095 1100 1105 1110

1115 1120 1125

1130 1135 1140

1145 1150 1155

1160 1165 1170

1175 1180 1185 1190

1205

1220

1235

1250

1270

1285

Val Lys Leu Asp Lys Lys Lys Asn Ala Tyr Tyr Ser His Val Ile Pro

1290	1295	1300	
aag gaa gtc ctg agc gag gtc ttt ggg aag gtt ttc cag aaa aac gtc			4109
Lys Glu Val Leu Ser Glu Val Phe Gly Lys Val Phe Gln Lys Asn Val			
1305	1310	1315	
agt cct cag acc ttc agg aag atg gtc gag gac gga aga ctc gat ccc			4157
Ser Pro Gln Thr Phe Arg Lys Met Val Glu Asp Gly Arg Leu Asp Pro			
1320	1325	1330	
gaa aag gcc cag agg ctc tcc tgg ctc att gag ggg gac gta gtg ctc			4205
Glu Lys Ala Gln Arg Leu Ser Trp Leu Ile Glu Gly Asp Val Val Leu			
1335	1340	1345	1350
gac cgc gtt gag tcc gtt gat gtg gaa gac tac gat ggt tat gtc tat			4253
Asp Arg Val Glu Ser Val Asp Val Glu Asp Tyr Asp Gly Tyr Val Tyr			
1355	1360	1365	
gac ctg agc gtc gag gac aac gag aac ttc ctc gtt ggc ttt ggg ttg			4301
Asp Leu Ser Val Glu Asp Asn Glu Asn Phe Leu Val Gly Phe Gly Leu			
1370	1375	1380	
gtc tat gct cac aac agc tac tac ggt tac tac ggc tat gca agg gcg			4349
Val Tyr Ala His Asn Ser Tyr Tyr Gly Tyr Tyr Gly Tyr Ala Arg Ala			
1385	1390	1395	

cgc tgg tac tgc aag gag tgt gca gag agc gta acg gcc tgg gga agg 4397

Arg Trp Tyr Cys Lys Glu Cys Ala Glu Ser Val Thr Ala Trp Gly Arg

1400

1405

1410

gag tac ata acg atg acc atc aag gag ata gag gaa aag tac ggc ttt 4445

Glu Tyr Ile Thr Met Thr Ile Lys Glu Ile Glu Glu Lys Tyr Gly Phe

1415

1420

1425

1430

aag gta atc tac agc gac acc gac gga ttt ttt gcc aca ata cct gga 4493

Lys Val Ile Tyr Ser Asp Thr Asp Gly Phe Phe Ala Thr Ile Pro Gly

1435

1440

1445

gcc gat gct gaa acc gtc aaa aag aag gct atg gag ttc ctc aag tat 4541

Ala Asp Ala Glu Thr Val Lys Lys Lys Ala Met Glu Phe Leu Lys Tyr

1450

1455

1460

atc aac gcc aaa ctt ccg ggc gcg ctt gag ctc gag tac gag ggc ttc 4589

Ile Asn Ala Lys Leu Pro Gly Ala Leu Glu Leu Glu Tyr Glu Gly Phe

1465

1470

1475

tac aaa cgc ggc ttc ttc gtc acg aag aag aag tat gcg gtg ata gac 4637

Tyr Lys Arg Gly Phe Phe Val Thr Lys Lys Lys Tyr Ala Val Ile Asp

1480

1485

1490

095592.051001

1495 1500 1505 1510

1515 1520 1525

1530 1535 1540

1545 1550 1555

1560 1565 1570

1575 1580 1585 1590

cct gga acg gtg ata agc tac atc gtg ctc aag ggc tct ggg agg ata 4973

Pro Gly Thr Val Ile Ser Tyr Ile Val Leu Lys Gly Ser Gly Arg Ile

1595

1600

1605

ggc gac agg gcg ata ccg ttc gac gag ttc gac ccg acg aag cac aag 5021

Gly Asp Arg Ala Ile Pro Phe Asp Glu Phe Asp Pro Thr Lys His Lys

1610

1615

1620

tac gac gcc gag tac tac att gag aac cag gtt ctc cca gcc gtt gag 5069

Tyr Asp Ala Glu Tyr Tyr Ile Glu Asn Gln Val Leu Pro Ala Val Glu

1625

1630

1635

aga att ctg aga gcc ttc ggt tac cgc aag gaa gac ctg cgc tac cag 5117

Arg Ile Leu Arg Ala Phe Gly Tyr Arg Lys Glu Asp Leu Arg Tyr Gln

1640

1645

1650

aag acg aga cag gtt ggt ttg agt gct tgg ctg aag ccg aag gga act 5165

Lys Thr Arg Gln Val Gly Leu Ser Ala Trp Leu Lys Pro Lys Gly Thr

1655

1660

1665

1670

tgacctttcc atitgttttc cagcggataa ccctttaact tccctttcaa aaactccctt 5225

tagggaaaga ccatgaagat agaaatccgg cggcgcccgg ttaaatacgc taggatagaa 5285

gtgaagccag acggcagggt agtcgtcact gccccgaggg ttcaacgttg agaagtt 5342

09852922 051001

<211> 774

〈213〉 *Pyrococcus kodakaraensis*

Met Ile Leu Asp Thr Asp Tyr Ile Thr Glu Asp Gly Lys Pro Val Ile

1 5 10 15

Arg Ile Phe Lys Lys Glu Asn Gly Glu Phe Lys Ile Glu Tyr Asp Arg

20 25 30

Thr Phe Glu Pro Tyr Phe Tyr Ala Leu Leu Lys Asp Asp Ser Ala Ile

35 40 45

Glu Glu Val Lys Lys Ile Thr Ala Glu Arg His Gly Thr Val Val Thr

50 55 60

Val Lys Arg Val Glu Lys Val Gln Lys Lys Phe Leu Gly Arg Pro Val

65 70 75 80

Glu Val Trp Lys Leu Tyr Phe Thr His Pro Gln Asp Val Pro Ala Ile

85 90 95

Arg Asp Lys Ile Arg Glu His Pro Ala Val Ile Asp Ile Tyr Glu Tyr

100

105

110

Asp Ile Pro Phe Ala Lys Arg Tyr Leu Ile Asp Lys Gly Leu Val Pro

115

120

125

Met Glu Gly Asp Glu Glu Leu Lys Met Leu Ala Phe Asp Ile Glu Thr

130

135

140

Leu Tyr His Glu Gly Glu Glu Phe Ala Glu Gly Pro Ile Leu Met Ile

145

150

155

160

Ser Tyr Ala Asp Glu Glu Gly Ala Arg Val Ile Thr Trp Lys Asn Val

165

170

175

Asp Leu Pro Tyr Val Asp Val Val Ser Thr Glu Arg Glu Met Ile Lys

180

185

190

Arg Phe Leu Arg Val Val Lys Glu Lys Asp Pro Asp Val Leu Ile Thr

195

200

205

Tyr Asn Gly Asp Asn Phe Asp Phe Ala Tyr Leu Lys Lys Arg Cys Glu

210

215

220

Lys Leu Gly Ile Asn Phe Ala Leu Gly Arg Asp Gly Ser Glu Pro Lys

FOOTER: 2262560

225 230 235 240

Ile Gln Arg Met Gly Asp Arg Phe Ala Val Glu Val Lys Gly Arg Ile

245 250 255

His Phe Asp Leu Tyr Pro Val Ile Arg Arg Thr Ile Asn Leu Pro Thr

260 265 270

Tyr Thr Leu Glu Ala Val Tyr Glu Ala Val Phe Gly Gln Pro Lys Glu

275 280 285

Lys Val Tyr Ala Glu Glu Ile Thr Thr Ala Trp Glu Thr Gly Glu Asn

290 295 300

Leu Glu Arg Val Ala Arg Tyr Ser Met Glu Asp Ala Lys Val Thr Tyr

305 310 315 320

Glu Leu Gly Lys Glu Phe Leu Pro Met Glu Ala Gln Leu Ser Arg Leu

325 330 335

Ile Gly Gln Ser Leu Trp Asp Val Ser Arg Ser Ser Thr Gly Asn Leu

340 345 350

Val Glu Trp Phe Leu Leu Arg Lys Ala Tyr Glu Arg Asn Glu Leu Ala

355 360 365

09552922"051001
T00T50"22225860

Pro Asn Lys Pro Asp Glu Lys Glu Leu Ala Arg Arg Arg Gln Ser Tyr

370

375

380

Glu Gly Gly Tyr Val Lys Glu Pro Glu Arg Gly Leu Trp Glu Asn Ile

385

390

395

400

Val Tyr Leu Asp Phe Arg Ser Leu Tyr Pro Ser Ile Ile Ile Thr His

405

410

415

Asn Val Ser Pro Asp Thr Leu Asn Arg Glu Gly Cys Lys Glu Tyr Asp

420

425

430

Val Ala Pro Gln Val Gly His Arg Phe Cys Lys Asp Phe Pro Gly Phe

435

440

445

Ile Pro Ser Leu Leu Gly Asp Leu Leu Glu Glu Arg Gln Lys Ile Lys

450

455

460

Lys Lys Met Lys Ala Thr Ile Asp Pro Ile Glu Arg Lys Leu Leu Asp

465

470

475

480

Tyr Arg Gln Arg Ala Ile Lys Ile Leu Ala Asn Ser Tyr Tyr Gly Tyr

485

490

495

09652923 051001
100159 22629860

Tyr Gly Tyr Ala Arg Ala Arg Trp Tyr Cys Lys Glu Cys Ala Glu Ser

500

505

510

Val Thr Ala Trp Gly Arg Glu Tyr Ile Thr Met Thr Ile Lys Glu Ile

515

520

525

Glu Glu Lys Tyr Gly Phe Lys Val Ile Tyr Ser Asp Thr Asp Gly Phe

530

535

540

Phe Ala Thr Ile Pro Gly Ala Asp Ala Glu Thr Val Lys Lys Lys Ala

545

550

555

560

Met Glu Phe Leu Lys Tyr Ile Asn Ala Lys Leu Pro Gly Ala Leu Glu

565

570

575

Leu Glu Tyr Glu Gly Phe Tyr Lys Arg Gly Phe Phe Val Thr Lys Lys

580

585

590

Lys Tyr Ala Val Ile Asp Glu Glu Gly Lys Ile Thr Thr Arg Gly Leu

595

600

605

Glu Ile Val Arg Arg Asp Trp Ser Glu Ile Ala Lys Glu Thr Gln Ala

610

615

620

Arg Val Leu Glu Ala Leu Leu Lys Asp Gly Asp Val Glu Lys Ala Val

09552922.051001
T00T50.2255550

625	630	635	640
Arg Ile Val Lys Glu Val Thr Glu Lys Leu Ser Lys Tyr Glu Val Pro			
645	650	655	
Pro Glu Lys Leu Val Ile His Glu Gln Ile Thr Arg Asp Leu Lys Asp			
660	665	670	
Tyr Lys Ala Thr Gly Pro His Val Ala Val Ala Lys Arg Leu Ala Ala			
675	680	685	
Arg Gly Val Lys Ile Arg Pro Gly Thr Val Ile Ser Tyr Ile Val Leu			
690	695	700	
Lys Gly Ser Gly Arg Ile Gly Asp Arg Ala Ile Pro Phe Asp Glu Phe			
705	710	715	720
Asp Pro Thr Lys His Lys Tyr Asp Ala Glu Tyr Tyr Ile Glu Asn Gln			
725	730	735	
Val Leu Pro Ala Val Glu Arg Ile Leu Arg Ala Phe Gly Tyr Arg Lys			
740	745	750	
Glu Asp Leu Arg Tyr Gln Lys Thr Arg Gln Val Gly Leu Ser Ala Trp			
755	760	765	

Leu Lys Pro Lys Gly Thr

770

<210> 3

<211> 2325

<212> DNA

<213> *Pyrococcus kodakaraensis*

<400> 3

atgatactcg acactgacta cataaccgag gatggaaagc ctgtcataag aattttcaag 60
aaggaaaacg gcgagttaa gattgagtac gaccggactt ttgaacccta cttctacgcc 120
ctcctgaagg acgattctgc cattgaggaa gtcaagaaga taaccgccga gaggcacggg 180
acggttgtaa cggttaagcg ggttgaaaag gttcagaaga agttcctcgg gagaccagtt 240
gaggctcgga aactctactt tactcatccg caggacgtcc cagcgataag ggacaagata 300
cgagagcatc cagcagttat tgacatctac gatlacgaca tacccttcgc caagcgtac 360
ctcatagaca agggattagt gccaatggaa ggcgacgagg agctgaaaat gctcgccctc 420
gacattgaaa ctctctacca tgagggcgag gatttcgccg aggggccaat ctttatgata 480
agctacgccg acgaggaagg ggccagggtg ataacttgga agaacgtgga tctcccctac 540
gttgacgtcg tctcgacgga gagggagatg ataaagcgct tcctccgtgt tgtgaaggag 600
aaagacccgg acgttctcat aacctacaac ggcgacaact tcgacttcgc ctatctgaaa 660
aagcgctgtg aaaagctcgg aataaacttc gccctcggaa gggatggaag cgagccgaag 720
attcagagga tgggcgacag gtttgccgtc gaagtgaagg gacggataca cttcgatctc 780
tatcctgtga taagacggac gataaacctg cccacataca cgcttgaggc cgtttatgaa 840

094522 051004

gccgtcttcg gtcagccgaa ggagaagggt tacgctgagg aaataaccac agcctgggaa 900
 accggcgaga accttgagag agtcgcccgc tactcgatgg aagatgcgaa ggtcacatac 960
 gagcttggga aggagttcct tccgatggag gccagcttt ctcgcttaat cggccagtc 1020
 ctctgggacg tctcccgc cagcactggc aacctcggtg agtggttcct cctcaggaag 1080
 gcctatgaga ggaatgagct ggccccgaac aagcccgatg aaaaggagct ggccagaaga 1140
 cggcagagct atgaaggagg ctatgtaaaa gagcccgaga gagggttgtg ggagaacata 1200
 gtgtacctag atttiagate cctgtacccc tcaatcatca tcaccacaa cgtctcgccg 1260
 gatacgctca acagagaagg atgcaaggaa tatgacgttg cccacaggt cggccaccgc 1320
 ttctgcaagg acttcccagg atttatcccg agcctgcttg gagacctcct agaggagagg 1380
 cagaagataa agaagaagat gaaggccacg attgaccga tcgagaggaa gctcctcgat 1440
 tacaggcaga gggccatcaa gatectggca aacagctact acggttacta cggctatgca 1500
 agggcgcgct ggtactgcaa ggagtgtgca gagagcgtaa cggcctgggg aaggagtag 1560
 ataacgatga ccatcaagga gatagaggaa aagtacggct ttaaggtaat ctacagcgac 1620
 accgacggat tttttgccac aataccigga gccgatgctg aaaccgtcaa aaagaaggct 1680
 atggagtcc tcaagtatat caacgccaaa ctccggggcg cgcttgagct cgagtacgag 1740
 ggcttctaca aacgcggctt ctccgtcacg aagaagaagt atgcggtgat agacaggaa 1800
 ggcaagataa caacgcgagg acttgagatt gtgaggcgtg actggagcga gatagcga 1860
 gagacgcagg cgagggttct tgaagcittg cttaaaggacg gtgacgtcga gaaggccgtg 1920
 aggatagtca aagaagttac cgaaaagctg agcaagtagc aggttccgcc ggagaagctg 1980
 gtgatccacg agcagataac gagggattta aaggactaca aggcaaccgg tccccagtt 2040
 gccgttgcca agaggttggc cgcgagagga gtcaaaatac gccctggaac ggtgataagc 2100
 tacatcgtgc tcaagggctc tgggaggata ggcgacaggc cgataccgtt cgacgagttc 2160
 gacccgacga agcacaagta cgacgccgag tactacattg agaaccaggt tctcccagcc 2220
 gttgagagaa ttctgagac ctccggttac cgcaaggaag acctgcgcta ccagaagacg 2280
 agacaggttg gttgagtagc ttggctgaag ccgaaggga cttga 2325

<210> 4

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 4

gaaactctct acgaggaggg cgaggagttc gccg

34

<210> 5

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 5

cggcgaactc ctgcacctcc tcgtagagag ttic

34

<210> 6

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 6

gaaactctct acgacgaggg cgaggagttc gccg

34

<210> 7

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 7

cggcgaactc ctgcacctcg tcgtagagag ttic

34

<210> 8

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 8

gaaactctct actacgaggg cgaggagttc gccg

34

<210> 9

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 9

cggcgaactc ctgcacctcg tagtagagag ttic

34

<210> 10

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 10

gaaactctct acgccgaggg cgaggagttc gc

32

<210> 11

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 11

gcgaactcct cgccctcggc gtagagagtt tc

32

<210> 12

<211> 30

1.00T50" 22625850

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 12

gaaactctct acaaggaggg cgaggagttc

30

<210> 13

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 13

gaactcctcg cctccttgt agagagtttc

30

<210> 14

<211> 32

<212> DNA

09852993.051001

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 14

aaagctctct acagggaggg cgaggagttc gc

32

<210> 15

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 15

gcgaactcct cgccctccct gtagagagtt tc

32

<210> 16

<211> 34

<212> DNA

<213> Artificial Sequence

09552922.051001

<220>

<223> Description of Artificial Sequence:primer

<400> 16

gaaactctct actctgaggg cgaggagttc gccg

34

<210> 17

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 17

cggcgaactc ctgcacctca gagtagagag ttic

34

<210> 18

<211> 34

<212> DNA

<213> Artificial Sequence

100T50-2252360

<220>

<223> Description of Artificial Sequence:primer

<400> 18

gaaactctct accaggaggg cgaggagttc gccg

34

<210> 19

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 19

cggcgaactc ctcgccctcc tggtagagag ttic

34

<210> 20

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

095592-051001

<223> Description of Artificial Sequence:primer

<400> 20

ggtgttcct tgatgtagca ca

22

<210> 21

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 21

acatgtatit gcatggaaaa caactc

26

<210> 22

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 22

agtgccttcgt gcccgatgac

20

<210> 23

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 23

tgccccttgg tgacatactc g

21

<210> 24

<211> 35

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

05352923-054001
T00T50-2262580

<400> 24

aaaaacgcgt caccagtcac agaaaagcat ctac

35

<210> 25

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 25

aaaaacgcgt caaccaagtc attctgagaa tagt

34

<210> 26

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 26

TOP SECRET

25

⟨213⟩ Artificial Sequence

<223> Description of Artificial Sequence:primer

gagggcagaa gtttattccg agctt

⟨213⟩ Artificial Sequence

<223> Description of Artificial Sequence:primer

cgccagggtt ttcccagtca cgac

24